

PATENT  
USSN 08/974,584  
015389-002950US  
018/206p2

**APPENDIX A****BEST AVAILABLE COPY****Mouse TERT protein sequence**

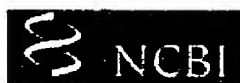
LOCUS 070372 1122 aa linear ROD 15-JUN-2002  
DEFINITION Telomerase reverse transcriptase (Telomerase catalytic subunit).  
ORGANISM Mus musculus  
AUTHORS Greenberg,R.A., Allsopp,R.C., Chin,L., Morin,G.B. and DePinho,R.A.  
TITLE Expression of mouse telomerase reverse transcriptase during  
development, differentiation and proliferation  
JOURNAL Oncogene 16 (13), 1723-1730 (1998)

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1 mtraprcpav rsllrsryre vwplatfvrr lgpegrrlvq pgdpkiyrtl vaqclvcmh  
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121 sylvntviet lrvsgawmll lsrvgdllv yllahcalyl lvppscayqv cgsplyqica  
181 ttidiwpsvsa syrptrpvgr nftnlrflqq iksssrqcap kplalpsrgt krhlsltsts  
241 vpsakkarcy pvprveegph rqvlptpsgk swvpsparsp evptaekdls skgkvsdls  
301 sgsvcckhkp sstslsppr qnafqlrpfi etrhflysrg dgqerlnpsf llsnlqpnlt  
361 garrlveiff lgsrprtsqp lcrthrlsrr ywqmrplfq llnvhaecqy vlllrshcrf  
421 rtanqqvtda lntspplmd lirlhsspwq vygfllracic kvvsaslwgt rhnerrffkn  
481 lkkfislgyk gklslqelmw kmkvedchw l rsspdkdrvp aaehrlreri latflfwlmd  
541 tyvvqlrsf fyitestfqq nrlffyrksv wsklqsigvr qhlervrlre lsqeevrhhq  
601 dtwlampicr lrfipkngl rpivnmsysm gtralgrrkq aqhftqrlkt lfsmlnyert  
661 khphlmgssv lgmndlyrtw rafvlrvral dqtprmyfvk advtgaydai pggklvevva  
721 nmirhsesty cirqyavvrr dsqggvhksf rrqvtllsd l qpymgqflkh lqdsdasalr  
781 nsvvieqsis mnessssldf fflhflrhsv vkigdrctyq cggipqgssl stllcslcf  
841 dmenklfaev qrdglllrffv ddfllvtphl dqaktflstl vhgvpaygcm inlqktvvnf  
901 pvepgtlgga apyqlpahcl fpwcgllldt qtlevfcdys gyaqtsikts ltfqsvfkag  
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1021 nltffligiis sqasccyail kvknpgmtlk asgsfppeaa hwlcycqafll klaahsviyk  
1081 cllgplrtaq klckrlpea tmtilkaaad palstdfqi ld
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## SEQ. ID NO:124 (Figure 60)

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TCTTCAAAGC TGGGAAGACC ATGCGGAACA AGCTCCTGTC GGTCTGCGG TTGAAGTGT 3000
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# ORF Finder (Open Reading Frame Finder)

PubMed

Entrez

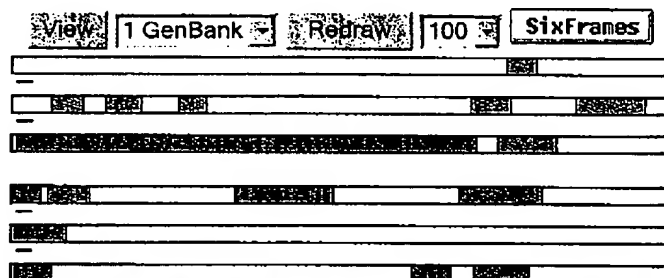
BLAST

OMIM

Taxonomy

Structure

## Anonymous

Program ☒ blastp Database ☐ nr ☒ BLAST ☐ with parameters ☒ Cognitor

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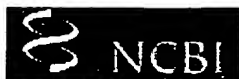
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L G P E G R R L V Q P G D P K  
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G S Q P P P A D L S F H Q V S  
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S L K E L V A R V V Q R L C E  
303 cgcaacgagagaaaacgtgctggtgttttggctttgagctgcttaac  
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S Y L P N T V I E T L R V S G  
438 gcatggatgctactgttgagccgagtgggcgacgacctgctggtc  
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Y L L A H C A L Y L L V P P S  
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T T D I W P S V S A S Y R P T  
618 cgacccgtgggcagggaatttcactaaccttaggttcttacaacag  
R P V G R N F T N L R F L Q Q  
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Frame from to Length

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-2	1..258	258
-1	170..370	201
-3	1..191	191
+2	2117..2302	186
-3	1842..2018	177
+2	440..604	165
+2	191..337	147
-1	2..139	138
+1	2281..2415	135
+2	776..907	132

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V P S A K K A R C Y P V P R V  
798 gaggaggacccccacaggcagggtgctaccaaccccatcaggcaaa  
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843 tcatgggtgccaagtccctgctcgggtcccccagggtgctactgca  
S W V P S P A R S P E V P T A  
888 gagaaagatttgtcttcttaaaggaaaggtgtctgacctgagttct  
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933 tctgggtcgggtgtgctgtaaacacaaagcccagctccacatctctg  
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L S P P R Q N A F Q L R P F I  
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1068 ctaaacccctcattcctactcagcaacctccagcctaacttgact  
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2013 aaacatcctcaccttatgggggtcttctgtactgggtatgaatgac

K H P H L M G S S V L G M N D  
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## Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

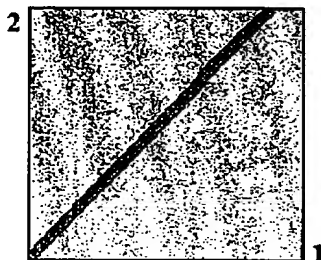
Structure

### BLAST 2 SEQUENCES RESULTS VERSION TBLASTN 2.2.13 [Nov-27-2005]

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x\_dropoff: **50** expect: **10.000** wordsize: **3** Filter ☐ View option **Standard**  
Masking character option **X for protein, n for nucleotide** Masking color option **Black**  
☐ Show CDS translation **Aug**

Sequence 1: lcl|seq\_1  
Length = 1122 (1 .. 1122)

Sequence 2: lcl|seq\_2  
Length = 3025 (1 .. 3025)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score = 1595 bits (4129), Expect = 0.0  
Identities = 830/1001 (82%), Positives = 840/1001 (83%), Gaps = 22/1001 (2%)  
Frame = +3

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Sbjct	33	MTRAPRCPAVRSLLRSRYREVWPLATFVRRLGPEGRRLVQPGDPKIYRTLVAQCLVCMHW	212
Query	61	GSQPPPADLSFHQVSSLKELVARVVQRLCERNERNVLAFGFELLNEARGGPPMAFTSSVR	120
Sbjct	213	GSQPPPADLSFHQVSSLKELVARVVQRLCERNERNVLAFGFELLNEARGGPPMAFTSSVR	392
Query	121	SYLPNTVIETLRVSGAWMLLLSRVGDDLLVYLLAHCALYLLVPPSCAYQVCGSPLYQICA	180
Sbjct	393	SYLPNTVIETLRVSGAWMLLLSRVGDDLLVYLLAHCALYLLVPPSCAYQVCGSPLYQICA	572
Query	181	TTDIWPSVSASYRPTRPVGRNFTNLRFLQIQKSSSRQEAPKPLALPSRGTKRHLSTSTS	240
		TTDIWPSVSASYRPTRPVGRNFTNLRFLQIQKSSSRQEAPKPLALPSRGTKRHLSTSTS	

Sbjct	573	TTDIWPSVSASYRPTRPVGRNFTNLRFLQKSSSRQEAPKPLALPSRGTKRHLSLTSTS	752
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Sbjct	753	VPSAKKARCYFVPRVEEGPHRQVLPTPSGKSWVSPARSPEVPTAEKDLSSKGKVSDDL	932
Query	301	SGSVCCCHKPSSTSLSPPRQNAFQLRPFIEIETHFLYSRGDGQERLNPSFLLSNLQPNLT	360
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Sbjct	1653	TYVVQLLSFFYITESTFQKNRLFFYRKSVWSKLQSIGVRQHLEVRVRLRELSQEEVRHHQ	1832
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Sbjct	2721	XXXCSY	2900
Query	943	AQTSIKTSLTFQSVFKAGKTMRNKLLSVLRLKCHGLFLDLQ	983
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Lambda	K	H
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PATENT  
USSN 08/974,584  
015389-002950US  
018/206p2

**T motif encoded in SEQ. ID NO:124 mTRT fragment**

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mTERT:	61	GSQPPPADLSFHQVSSLKELVARVVQRLCERNERNVLAFGFELLNEARGGPPMAFTSSVR	120
SEQ. 124:	213	GSQPPPADLSFHQVSSLKELVARVVQRLCERNERNVLAFGFELLNEARGGPPMAFTSSVR	392
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SEQ. 124:	393	SYLPNTVIETLRVSGAWMLLSRVGDDLLVYLLAHCALYLLVPPSCAYQVC6SPLYQICA	572
mTERT:	181	TTDIWPSVSASYRPTRPVGRNFTNLRFLQQIKSSSRQEAPKPLALPSRGTKRHLSLTSTS	240
SEQ. 124:	573	TTDIWPSVSASYRPTRPVGRNFTNLRFLQQIKSSSRQEAPKPLALPSRGTKRHLSLTSTS	752
mTERT:	241	VPSAKKARCYPVPRVEEGPHRQVLPTPSGKSNVPSPARSPEVPTAEKDLSSKGKVS DLSL	300
SEQ. 124:	753	VPSAKKARCYPVPRVEEGPHRQVLPTPSGKSNVPSPARSPEVPTAEKDLSSKGKVS DLSL	932
mTERT:	301	SGSVCCCKHKPSSTSLSPPRQNAFQLRPF IETRHF LYSRGDGGQERLNPSFLLSNLQPNLT	360
SEQ. 124:	933	SGSVCCCKHKPSSTSLSPPRQNAFQLRPF IETRHF LYSRGDGGQERLNPSFLLSNLQPNLT	1112
mTERT:	361	GARRLVEIIFLGSRPRTSGPLCRTHRLSRRYWQMRPLFQQLLVNHAECQYVRLLRSHCRF	420
SEQ. 124:	1113	GARRLVEIIFLGSRPRTSGPLCRTHRLSRRYWQMRPLFQQLLVNHAECQYVRLLRSHCRF	1292
mTERT:	421	RTANQQVTDALNTSPPHLMDLLRLHSSPWQVYGFLRACLCKVVSASLWGTRHNERRFFKN	480
SEQ. 124:	1293	RTANQQVTDALNTSPPHLMDLLRLHSSPWQVYGFLRACLCKVVSASLWGTRHNERRFFKN	1472
mTERT:	481	LKKFISLGKYGKLSLQELMWKMKVEDCHWLRS SPGKDRVPAAEHRLRERILATFLFWEMD	540
SEQ. 124:	1473	LKKFISLGKYGKLSLQELMWKMKVEDCHWLRS SPGKDRVPAAEHRLRERILATFLFWEMD	1652
mTERT:	541	TYVVQLLRSEFFYITESTFOKNRFFYRKSVWSKLQSIGVROHLERVRLRELSQEEVRHHQ	600
SEQ. 124:	1653	TYVVQLLRSEFFYITESTFOKNRFFYRKSVWSKLQSIGVROHLERVRLRELSQEEVRHHQ	1832
mTERT:	601	DTWLAMPICRLRFIPKPNGLRPIVNMSYSMGTRALGRRKQAQHTQRLKTLFSMLNYERT	660
SEQ. 124:	1833	DTWLAMPICRLRFIPKPNGLRPIVNMSYSMGTRALGRRKQAQHTQRLKTLFSMLNYE T	2012
mTERT:	661	KPHLMGSSVLGMNDIYRTWRAFVLRVRALD	691
SEQ. 124:	2013	KPHLMGSSVLGMNDIYRTWRAFVLRVRALD	



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